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In Fig. 1 and in the stereomodels of antibody combining sites, the location of the allotypic regions may clearly be seen to be on the outside of  $V_{\text{H}}$  away from the combining site. Residues 9 and 65 of  $V_{\text{H}}$ are numbered and will facilitate location of the Vma allotypes. The few cDNA sequences available in 1984 (65) provided no evidence that germ line sequences encoding latent allotypes may exist in some rabbits. Since then, additional germline and expressed  $V_{\rm H}a$  sequences (63-65,188,204-206) have further refined the information on  $V_{\text{H}}a$  allotypes and  $V_{\text{H}}a^-$  sequences. Newer analyses of germline  $V_{\text{H}}$ genes of rabbits have provided examples of potential genes and pseudogenes which could generate latent allotype sequences by somatic gene conversion mechanisms (187,199,203-208). Antisera to rabbit  $V_{\text{H}}a$  allotypes crossreact with human IgG, various other species of IgM and IgG, and with the Galapagos shark 7S immunoglobulin and correlate with the N-terminal amino acid

It is becoming of great importance, with all of the different mechanisms which are clearly generating diversity, to evaluate the extent to which each type of diversity, other than those resulting in pseudogenes, contributes noise rather than functional differences in complementarity of antibody combining sites (70,

Ohno et al. (212,213) have proposed that the genes coding for variable domains of the light and heavy chains arose from tandem repeats of a primordial nucleotide sequence about 48 base pairs in repeats of a primordial nucleotide sequence about 48 base pairs in length which subsequently diverged by mutations and deletions producing a resemblance to FRI, FR2, and FR3. The complementary strand of the primordial 48 base pair repeat of V<sub>L</sub> became the primordial V<sub>R</sub>. The finding (147) that the complementary strands of the human D2 and D4 minigenes coded for a portion of CDR1 of V<sub>R</sub> building block has also been proposed for the gene for the class I major histocompatibility complex (214):

The format of our precursor, V-region, C region sequences etc. of antibodies and T cell receptors has proven very useful in selecting primers for the polymerase chain reaction (215-217).

Constant Region Sequences

The constant region sequences were aligned in such a manner as to permit various comparisons of the light chain  $(C_L)$  and the individual domains of the heavy chain  $(C_R1, C_R2, C_R3, \text{ and } C_R4)$ . This was accomplished by sequential numbering on the left with gaps inserted for alignment. The following numbering system is used:

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108 to 215 of C<sub>L</sub>;
114 to 223 of C_{\rm H}1, plus the first part of hinge (224 to 241),
                      the end of hinge (242 and 243), and the
                      first two residues of CH2 (244 and 245);
246 to 360 of C<sub>#</sub>2;
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361 to 496 of C<sub>8</sub>3; 497 to 628 of CH4.

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The gene quadruplication in the human IgG3 hinge region (218) is numbered differently using letters 241A to 241Z, and 241AA to 241SS, and these residues should not be used in aligning domains for homology. The next two columns in the heavy chain tables indicate the EU (67) and OU (219) residue numbers, respectively. The succeeding columns which are numbered give the sequence data. The  $C_R$  and hinge domains conform to the findings of Sakano et al. (220), who defined each domain precisely by sequencing the coding and intervening nucleotide sequences bordering each domain.

The extensive nucleotide sequence data on exons for the constant regions of heavy chains have provided exact boundaries for  $C_{H}1$ , hinge,  $C_{H}2$ ,  $C_{H}3$ , and  $C_{H}4$ . Usually the introns separating these domains fall within the codon for a single amino acid. We have included that amino acid residue with the domain, the exon of which contains two of the three coding nucleotides. The constant regions

	Y CONST.	OU	IAIMS CB2 INVARIANT RESIDUES	HUMAI IGM CL	N HUMA IGM				x15115	679 GLI	CL	WAB	•	11 ERI H		13 HUMAN IGD MEMB 'CL	14 HUMAN IGG3'C	OMM	HEB	17 FRO	18 JON	19 MIS
243A 243B 243C 243D 243E 243F 243G 243H 243I 244	231 232	230 231 232	VAL PRO SER THR PRO PRO	VAL	VAL	VA.	L VAL	VAL	VAL VAL ALA								ALA PRO		ALA			
245A 245B 245C 246 247 248 249 250 251 251A	233 234 235 236 237 238	233 234 235 236 237 238	PRO	GLU LEU PRO PRO LYS VAL	GLU LEU PRO PRO LYSL VAL	GL.	M GLU U LEU O PRO O PRO S LYS L VAL	GLU PRO PRO LYS VAL	GLU LEU PRO PRO LYS VAL	,	1	SER HIS THR GLN PRO LEU	HIS THR GLN PRO LEU		SER HIS THR GLN PRO LEU		GLU LEU LEU GLY GLY PRO	GLU LEU LEU GLY PRO	GLU LEU LEU GLY	GLU LEU LEU GLY GLY	GLU LEU GLY GLY	GLU LEU LEU
222534 5522554 556789 012234 566789 022222 22222 22222 22222 22222 22222 2222	239 240 241 2443 2445 245 247 2489 250 251 255 255 255 255 255 257	239 240 241 242 243 244 245 246 247 249 250 255 255		SER VAL PHE VAL PRO	SER VAL PHE VAL PRO ARG ASP PHE GLY ASN PRO ARG LYS	VALUE PHI ASS PRI ASS	E PHE L VAL O PRO O PRO O ARG P ASX P GLY E PHE P HE P HE P HE P HE P HE P HE P H	PHE VAL PRO ARG ASP PHE PHE GLY ASN PRO ARG ARG SER	SER VAL PHE PRO ARG ASLY PHE PHE PHE PHE PHE PHE PHE PHE SER SER SER	•		GLY VAL TYR LEU LEU THR PRO ALA VAL GLN GLN TRP LEU TRP LEU ARG ASP LYS	VAL TYR LEU LEU THR PRO ALA VAL GLIN GASP LEU TRP		GLY VAL TYR LEU LEU LHR PRO ALA VAL GLN GLN LEU LEU ASP LEU ASP LEU ASP LEU ASP LEU ASP ALA		SEAL LEUE PHOOP LYS PATHEU THE LEUE ARREST LEUE METERS ARREST PRO	PHE LEU PHO PRO LYS PRO LYS ASP THR LEU MET ILE	SER VAL PHE LEU PRO LYS PRO LYS ATHR LEU MET ILE SER	PHE LEU PHE PRO LYS PRO LYS ASP THR LEU MET ILE	PHE LEU PHE PRO PRO LYS PRO LYS ASP THR LEU MET ILE SER	PHE LEU PHO PRO PRO LYS PRO LYS LYS LYS LEU MET LEU MET LEU MET LER ARG THR
2222 27777 77777 5 777777 8 777777 8 777777 8 72822 2 72823 4 72823 4 7283 7	2589 2589 269 2664 2664 2669 2771 2774 2774	256 257 258 259 260 261 262 263 264 265 266 267 268	CYS	LYS LEU ILE CYS GLN ALA THR GLY PHE SER PRO GLN ILE GLN VAL	LYS LEU ILE CYS GLN ALA THR GLY PHE SER ARG GLN ILE GLN VAL	LY: LET	LYS LEU	LYS LEU ILE CYS GLN ALA THY PHE SER PRO GLN ILE GLU	LYS LEU LLE CYS GLN ALA THR GLY PHE SER PRO ARG GLN LLE GLN VAL		FINES ALLIA	THR PHE ITHR CYS ( PH	THR PHE PHE VAL VAL SLY SER ASP LEU LYS ASP		THE THE THE CYS PHE VALL GLY SER LEYS ASP LEYS ALA HIS		PRO GLU VAL THR CYAL VAL VAL VAL VAL ASP VAL SER HIS GLU ASP PRO GLU GLN	PRO GLU THR CYS VAL VAL VAL ASP PRO VAL GLU ASP PRO VAL			;	PRO GLU THR CYAL VAL VAL VASP VAL SER GLU PSPO GLU VALN VAL
288 289 2991 2991 2993 2994 2996 2998 2998 3001 3003	275 276 2778 2778 279 280 281 282 283 284 286 286 287	270 271 272 273 274 275 276 277 278 279 280 281 282 283 284	GLY(.95)	SER TRP LEU ARG GLU GLY LYS GLY SER GLY VAL GLY VAL THR		GLYS GLY GLY VAI GLY VAI THE	SER J LEU GARG J GLU GLY GLY SER J GLY VAL VAL THR	GLU GLY LYS GLN VAL GLY SER GLY VAL THR	SER TRP LEU ARG GLU GLY LYS GLN VAL GLY SER GLY VAL THR		T T T G V A G L - V P T G G V	THE	THR TRP SLU LA		THR TRP GLU VAL ALA GLYS VAL PRO THR GLY VAL		PHE LYS TRP TYR VAL  ASP GLY VAL GLU VAL HIS ASN ALA	PHE LYS TRP TYR VAL  ASP GLY VAL GLU VAL HIS ASN ALA	-			PHE LYS TRP VAL ASP GLY VAL GLN VAL HIS VAL
105 106 107 108 109 110 111 112 113	288 289 290 291 292 293 294 295 296	285 2867 2889 2991 2993 2993 2996		ASP GLN VAL GLN ALA GLU ALA LYS GLU SER GLU	ASP GLN VAL GLN ALA GLU ALA LYS GLU SER GLY PRO	GLX ALA LYS GLU	ASX GLX VAL GLX ALA LYS GLX SER GLY PRO	GLU ALA LYS GLU	ASP GLN VAL GLU ALA LYS GLU SER GLY		GLL GAHS	SN A	LU LEU LEU LRG IIS IER LSN		GLU GLY LEU LEU ARG HIS SER		LYS THR LYS PRO ARG GLU GLU GLU GLY TYR ASN	LYS THR LYS LEU ARG GLU GLU GLU TYR 		-		LYS FHR LYS PRO ARG SLU SLN PHE LSN
1678 90123 45678 90:23	299 300 301 302 303 304 305 306 307 309	296 297 298 299 3001 3002 3003 3005 3005 3006 3006 3006 3006 3008 3009 3111 3113	SER (.95)	PRO THR THR TYR LYS VAL THR SER THR LEU LYS GLU	THR TYSLVAL THR LYSL THR SER LEU THR LEU THR LEU THR LEU THR LEU THR LEU THR ASP	THR THR TYS VAL THR SER THR LEU THR LEU THR SER THR LEU THR	THR THR LYS VAL THR SER THR LEU THR LEU LYS GLX SER ASP TRP LEU	THR THR TYS LYS VAL THR SER THR LEU SER THR LLEU SER TRP LEU LYS	PRO THR TYRS LYAL THR SER THR THR LEU THR SER THR LEU THE LYS GLUR ASP TRP LEU		GS GSGHS ALTTLIP ASSLIT	LY S GS G	LY LER LER LER SELISE REUR LER REUR REEU REEU REEU REEU REEU		GLY GLY GLN GSEN GLN GSEN ARG LEHR LEHR LEH ARG LEHR LEH LEH LEH LEH LEH LEH LEH LEH LEH LEH		SER PHE ARGL VALL SER VALL SER VALL HIS GLSP TRP LEU	SER THE ARGLVAL VAL VAL VAL VAL VAL VAL VAL VAL VAL			F AVVS VLTVL HGAT	EER HHE HE HE HE HE HE HE HE HE HE HE HE HE
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51A 52 53 54 55 56 57 58 59 50	333 334 335 336 337 338	332 333 334 335 336 337 338 339		ASN ALA SER SER MET CYS VAL PRO	ASN ALA SER SER MET CYS VAL PRO	ASX ALA SER SER MET CYS VAL	ASN ALA	ASN ALA SER SER ŒT CYS	ASN ALA SER SER MET CYS VAL PRO		LE ME AL LE AR GL	U LE	A A B B B B B B B B B B B B B B B B B B	A L MAL . A GP	EU ET LA EU RG EU RO LA		GLU LYS THR ILE SER LYS THR	GLU LYS THR ILE SER LYS ALA LYS			GI GI TF III	LU CS IR ER CR

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GLX GLU THR THR THR LEU LEU PRO PRO PRO
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ALA ALA LEU LEU
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HEAVY	CONSTA	NT CH	AIMS CB2	REGI	ON (cont	'd)					
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HEAVY	COMST	ANT CH	LATHS CE	2 REGI	Off (cont	(b)														
	EU	OUINDEX	CHIMPAN- ZEE CH4-14 (IGG1)	45 HUMAN IGA1 'CL	GORILLA IGAL'CL	47 HUMAN IGG'CL	48 HUMAN IGG2 'CL	49 TIL	50 ZIE	51 SA	52 PIG	53 HUMAI IGG4 'CL	54 VIN	55 HUMAN IGE C	56 HUMA IGE 'CL'	S7 N CHIMS IGE 'CL	58 ORAN- GUTAN IGE'C	0266 NI UZE6 NI	61 80	: B
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244	231 232		ALA PRO	PRO SER	PRO SER	THR THR	ALA PRO	ALA PRO		ALA		ALA PRO	ALA							
245A 245B 245C	222	233		THR PRO PRO	PRO PRO														- VA	. VA
246 247 248	233 234 235	234 235	GLU LEU LEU	THR PRO SER	THR PRO SER	GLU PRO LEU	VAL ALA	PRO VAL ALA				GLU PHE LEU	PHE	ARG ASP PHE	PHE	ARG ASP PHE	ARG ASP PHE		G PRO X PRO E PRO	PR
248 249 250 251	236 237 238	236 237 238	GLY GLY PRO	PRO SER CYS	PRO PRO CYS	GLY GLY Pro	GLY PRO	GLY PRO				GLY GLY PRO	GLY GLY PRO	THR PRO PRO	THR PRO PRO	THR	THR PRC PRC	THR TH PRO PR PRO PR	R PRO O PRO	PR
251A 251B 252 253 254	239	239	SER	HIS PRO	HIS PRO	SER	SER	SER				SER	SER	THR	THR	THR	THR	THR TH	- CYS - HIS R PRS	PR
255	240 241 242	240 241 242	VAL PHÉ LEU	ARG LEU SER	ARG LEU SER	VAL PHE LEU	PHE LEU	VAL PHE LEU				PHE LEU	VAL PHE LEU	VAL LYS ILE	VAL LYS ILE	VAL LYS VAL	VAL LYS ILE	VAL VA LYS LY ILE IL	L ARC S LEC E SEI	
256 257 258	243 244 245	243 244	PHE PRO PRO	HIS ARG	LEU HIS ARG	PHE PRO PRO	PHE PRO PRO	PHE PRO PRO				PHE PRO PRO	PHE PRO PRO	LEU GLN SER	LEU GLN SER	LEU GLN SER	LEU GLN SER	LEU LE GLN GL	U LEU X HIS R ARG	HI
259 260 261	246 247 248	245 246 247	LYS PRO LYS	PRO ALA LEU	PRO ALA LEU	LYS PRO LYS	PRO LYS	PRO LYS				LYS PRO LYS	LYS PRO LYS	SER CYS ASP	SER CYS ASP	SER CYS ASP	SER CYS ASP	SER SE	R PRO	PR
261 262 263 264	248 249 250 251	248 249	LYS ASP THR LEU	LEU GLU ASP LEU	GLU ASP LEU	ASP THR LEU	ASP THR LEU	ASP THR LEU				ASP THR LEU	ASP THR LEU	GLY GLY GLY	GLY GLY GLY	GLY GLY	GLY GLY GLY	GLY GL GLY LE GLY GL	X LEU Y GLU U ASE	GL
265 266 267	252 253 254	250 251 252	MET ILE SER	LEU LEU GLY	LEU LEU GLY	MET ILE SER	MET ILE SER	MET ILE	ILE SER			MET ILE SER	MET ILE	HIS PHE	HIS PHE	HIS Phe	HIS PHE	HIS HI PHE PH	S LEU	J LE
268 269	256	253 254	ARG THR	SER GLU	SER GLU	ARG THR	ARG THR	ARG THR	ARG THR			ARG	SER ARG THR	PRO PRO THR	PRO PRO THR	PRO PRO THR	PRO LEU THR	PRO PR PRO PR THR TH	SEF	L SE!
270 271 272 273	257 258 259 260	255 256 257 258	PRO GLU VAL	ALA ASN LEU	ALA ASN LEU	PRO GLU VAL	PRO GLU VAL	PRO GLU VAL THR	PRO GLU VAL			PRO GLU VAL	PRO GLU VAL	GLN LEU	GLN LEU	ILE GLN LEU	I LE GLN LEU	GLN GL LEU LE	E ALA K ASN U LEU	ALI ASI LEI
274 275	261 262	259 260	THR CYS VAL	THR CYS THR	THR CYS THR	THR CYS VAL	THR CYS VAL	CYS VAL	CYS			THR CYS VAL	THR CYS VAL	CYS LEU	CYS	CYS LEU	CYS LEU	CAS CA	-·THP	CYE
276 277 278	263 264 265	261 262 263	VAL VAL ASP	LEU THR GLY	LEU THR GLY	VAL VAL ASP	VAL VAL ASP	VAL VAL ASP	VAL VAL ASP			VAL VAL ASP	VAL VAL ASP VAL	VAL SER GLY	VAL SER GLY	VAL SER GLY	VAL SER GLY	VAL VA	L LEU	LEU
279 280 281	266 267 268	264 265 266 267	VAL SER HIS	ARG ASP	LEU ARG ASP	VAL SER HIS	VAL SER HIS	SER	VAL SER HIS			VAL SER GLN	VAL SER GLN	TYR	TYR	TYR	TYR	TYR TY	R LEU R ARG	LEU
282 283 284	269 270 271	267 268	GLU ASP PRO	SER	SER	GLU ASP PRO	GLU ASP PRO	GLU ASP	GLU ASP PRO			GLU ASP PRO	GLU ASP PRO	PRO	PRO	PRO	PRO	PRO PRO	- SER	ASF ALJ SEF
285 286 287	272 273 274	269	GLU VAL LYS	GLY VAL THR	GLY VAL THR	GLU VAL LYS	GLU VAL GLN	GLU VAL GLN	GLU VAL GLN			GLU VAL GLN	GLX	GLY THR ILE	GLY THR	GLY THR	GLY THR	GLY GLY	GLY	GLY ALA THE
288 289	275 276 277	270 271	PHE ASN TRP	PHE THR TRP	PHE THR TRP	PHE ASN	PHE ASN	PHE ASN	PHE ASN			PHE ASN	ASN	ASN ILE	ILE ASN ILE	ILE ASN ILE	ILE ASN ILE		PHE THR	THE
290 291 292 293	278 279	272 273 274	TYR VAL	THR	THR	TRP TYR VAL	TRP TYR VAL	TRP TYR VAL	TRP TYR VAL			TRP TYR VAL	TRP TYR VAL	THR TRP LEU	THR TRP LEU	THR TRP LEU	THR TRP LEU	THR THE TRP TRE LEU LEG	TRP PRO SER	TRP PRO SER
294 295 296 297 298	280 281	275 276 277 278	ASP GLY	SER SER	SER SER	ASP GLY	ASP GLY	ASP GLY	ASP GLY			ASP GLY	ASP GLY	GLU ASP	GLU ASP	GLU ASP	GLU ASP	GLU GLI	SER	SER
299 299	282 283	279 280 281	VAL	GLY.	GLY LYS	VAL GLU	VAL	VAL		:		VAL	VAL -	GLY GLN	GLY	GLY	GLY:	GLY GLY		
301 ( ) 302 303	284 285 286	282 283	VAL HIS ASN	SER ALA VAL	SER ALA VAL	VAL HIS ASN	VAL HIS ASN	VAL HIS ASN	VAL HIS			VAL HIS ASN	VAL HIS ASN	VAL	GLN VAL MET	GLN VAL MET	GLN VAL MET	GLN GLI VAL VAI MET MET	CCD	CFD
304 305 306 307	287 288 289	284 285 286	ALA LYS THR	GLN GLY PRO	GLU GLY PRO	ALA LYS THR	ALA LYS THR	LYS	ALA LYS THR			ALA LYS THR	ALA LYS THR	VAL ASP	ASP VAL ASP	ASP VAL ASP	ASP VAL ASP	ASP ASE	GLU GLY PRO	GLU
307 308 309	290 291 292	287 288 289	LYS PRO ARG	PRO GLU ARG	PRO GLU ARG	LYS PRO TRP	LYS PRO ARG		LYS. PRO			LYS PRO ARG	LYS PRO ARG	LEU SER THR	LEU SER THR	LEU SER THR	LEU SER THR	ASP ASP LEU LEU SER SER THR THE	PRO	PRO
310 311 312 313	293 294 295 296	290 291 292 293	GLU GLU GLN TYR	ASP LEU CYS GLY	ASP LEU CYS GLY	GLU GLU GLN TYR	GLU GLU GLN PHE	GLU GLU GLN PHE				GLU GLU GLN PHE	GLU GLU GLN PHE	ALA SER THR THR	ALA SER THR THR	ALA SER THR THR	ALA SER ALA THR	ALA ALA SER SER THR THR THR GLU	ASP LEU CYS	ASP LEU CYS
314 315 316	297	294 295 296	ASN	CYS	CYS	ASN	ASN	ASN				ASN	ASX	GLN GLU	GLN	GLN	GLN GLU	GLN SER		
316 317 318	298 299	296 297 298	SER THR			SER THR	SER THR	SER THR				SER THR	SER	GLY GLU LEU	GLY GLU LEU	GLY GLU LEU	GLY GLU LEU	GLY GLY GLU GLU LEU LEU		
319 320 321 322	300 301 302 303	299 300 301 302	TYR ARG VAL VAL	TYR SER VAL SER	TYR SER VAL SER	TYR HIS VAL VAL	PHE ARG VAL VAL	PHE ARG VAL	ARG VAL			TYR ARG VAL	TYR ARG VAL	ALA SER THR	ALA SER THR	ALA SER THR	ALA SER THR	ALA ALA SER SER THR THR	TYR SER VAL	TYR SER VAL
323 324 325	304 305	303 304	SER Val	SER VAL	SER VAL	SER VAL	ser Val	VAL SER VAL	SER Val			VAL SER VAL	VAL	GLN SER GLU	GLN SER GLU	GLN SEOR GLU	GLN SER GLU	GLN GLU SER SER GLU GLU	SER SER	SER
326 327 328	306 307 308 309	305 306 307 308	LEU THR VAL LEU	PRO GLY	LEU PRO GLY	THR VAL	THR VAL	THR VAL	LEU THR VAL			LEU THR VAL		LEU THR LEU	LEU THR LEU	LEU THR LEU	LEU THR LEU	LEU LEU THR THR LEU LEU SER SER	LEU	PEÓ
329 330 331	310 311	309	HIS GLN	CYS ALA GLU	CYS ALA GLU	VAL HIS GLN	HIS GLN	VAL 1 HIS I GLN (	HIS			HIS GLN		SER GLN LYS	SER GLN LYS	SER GLN LYS	SER GLN LYS	GLN GLN	ALA	ALA
332 333	312 313 314	310 311 312 313	ASP TRP LEU	PRO <b>TRP</b> ASN	PRO TRP ASN	asn TRP Leu	TRP LEU	TRP	LEU			ASP TRP LEU		LYS HIS TRP LEU	HIS TRP LEU	HIS TRP LEU	ARG TRP LEU	HIS HIS TRP TRP LEU LEU	TRIP	TRP
334 335 336	315 316	314 315	ASN GLY	HIS GLY	HIS	ASN GLY	ASN	ASP GLY	ASP			ASN GLY		SER ASP	SER ASP	SER	SER	SER SER	HIS	HIS
336 337 338 339	317 318 319	316 317 318	LYS GLU TYR	LYS THR PHE	LYS THR PHE	LYS GLU	GLU	LYS I	LYS			LYS GLU	LYS GLU	ARG THR	ARG THR	ASP ARG THR	ASP ARG THR	ASP ASP ARG ARG THR THR	GLU	GLU THR
339 340 341	320 321 322	319 320 321	LÝS CYS LÝS	THR CYS THR	THR CYS THR	TYR LYS CYS LYS	LYS CYS	TYR T LYS I CYS C LYS I	YS YS			LYS CYS	TYR LYS CYS	TYR THR CYS	TYR THR CYS	TYR THR CYS	TYR THR CYS	TYR TYR THR THR CYS CYS GLN GLU	PHE THR CYS	THR
342 343 344	323	322	VAL SER ASN	ALA ALA TYR	ALA ALA TYR	VAL SER	VAL SER	VAL V	AL SER			VAL SER	LYS VAL SER	GLN VAL THR	GLN VAL THR	GLN VAL THR	GLN VAL THR	GLN GLU VAL VAL THR THR		
345 346	325 326 327	324 325 326	ALA	PRO GLU	PRO GLU	ASN LYS GLY	LYS GLY	ASN A LYS I GLY C	YS LY			CLY GLY	ASN LYS GLY	TYR GLN GLY	TYR GLN GLY	TYR GLN GLY	TYR GLN GLY	TYR TYR GLN GLX GLY GLY	PRO	HIS PRO GLU
347 348 349 350	328 329 330 331	327 328 329 330	PRO ALA PRO	SER LYS THR PRO	SER LYS THR PRO	LEU PRO ALA PRO	PRO ALA	LEU I PRO P ALA A	RO			PRO SER	LEU PRO SER	HIS THR PHE	HIS THR PHE	GLY THR PHE	ASP THR PHE	HIS HIS THR THR PHE PHE	LYS THR	LEU LYS THR
51 51 <b>a</b>	332	331	ILE	LEU	LEU	ILE	ILE	PRO F	LE			ILE	SER ILE	GLU	GLU	GLU	GLU	GLU GLX	PRO Leu	PRO Leu
152 153 154 155	333 334 335 336	332 333 334 335	GLU LYS THR I <b>LE</b>	THR ALA THR	THR ALA THR	GLU LYS THR	THR	GLU G LYS I THR I	YS HR	T	YS HR	LYS THR	GLU LYS THR	ASP SER THR	ASP SER THR	ASP SER THR	ASP SER THR	ASP ASX SER SER THR THR	THR ALA ASN	THR ALA ASN
56 57	337	336 337	SER	SER	SER	ILE SER	SER :	ILE I	ER	_	ER	SER :	ILE SER	LYS CYS	LYS CYS	LYS LYS CYS	LYS LYS CYS	LYS LYS	ILE :	I LE THR
358 359 360	338 339 340	338 339	LYS ALA LYS	LYS SER	LYS SER	LYS THR LYS	THR '	LYS L THR T LYS L	HR	T	HR	LYS ALA	LYS ALA LYS	ALA	ALA	ALA	ALA	ALA ALA	LYS SER	LYS

	EU In	DEX INDE	63 IGA2 'CL	64 HUMAN IGA2 A2M(1) 'CL	65 HUMAN IGA2 A2M(2) 'CL	GE I	GH, CL,	IGM-b	MUTANT 102 CL	70 MOPC 104E	CL	72 HPC76	73 G8 CA 1.7	GATSO IG	76 IGD SECR	77 IGD MEMB	78 B1-8. DELTA1	79 MOUSE IGG3 'CL	BO IGG MEM
THE THERE WE WANT MAKE THE THE THE THE THE THE THE THE THE TH	258 258 258 261 261 279 266 287 277 277 277 277 277 277 277 277 277	233 233 234 235 236 237 237 238 239 241 242 243 244 244 247 247 247 247 247 247 247 250 250 260 260 260 270 270 270 270 270 270 270 270 270 27	LEUU GLOU ALSA LEUU LEUU SEER ALSE LEUU LEUU SEER ALSE LEUU LEUU AASSPAALA LEUU LEUU LEUU AASSPAALA LEUU LEUU LEUU LEUU LEUU LEUU LEUU	VALOU PROOPPROOF PROOF P	LEUU GEYR GUY ASNU LEUU SEYR GUY ASNU LEUU CHRY GUY ASNU LEUU CHRY FRONT CHRY FRONT CHRY GUY AND LEUU CHRY GUY GUY GUY GUY GUY GUY GUY GUY GUY GU	ALALA	ET PLANTE ENERGY EXECUTE THE HOUSE HERE. TO A STATE OF THE PLANTE HERE HERE HERE HERE HERE HERE HERE HE	LN HR CR CS LL LE R IR UR LE UR LE	GALLG STPF		GET-I APVII GALG STPGT TLUVI						COLL STRV - AA-L GVHTA T	PRO GLY	
329 330 331 332 333	311 312 313 314	313	ALA GLN PRO TRP ASN	GLN PRO TRP ASN	ALA GLI GLN ILI PRO ASI TRP TRI ASN LEI	LEU	LE	E P V U	GL IL AS TR LE	E P U	GI II AS TR LE	E P UP					GLI ASI TRO ME:		
334 335 337 338 339 341 343 343 343 345 347 345 347 345 351 351 351 353 353 355 357 357 359 360	315 316 317 318 329 321 322 322 323 324 325 326 327 328 329 331 331 332 333 334 335 336 337 338 337 338 339 337	315 316 317 318 319 320 321 322 322 322 322 322 322 322 322 322	LIA IIA IIA IIA IIA IIA IIA IIA IIA IIA	GLU THR THR THR ALA ALA HIS HIS GLU CYS THR ALA ALA ALA ALA ALA ALA ALA ALE ALE ALE	HIS ASSIGNATION AS	LEU LEU LYS ARG GLY LEU LEU LYS	ASIA ASIA ASIA ASIA ASIA ASIA ARGILYS  ASIA ARGILY  ARGILY	N LRRSG LOSGE JAMES	AS: LEE VAI THI THI ARR VAI ASI ARR VAI ASI ARR ARR CGLY LEU LYS ASI ASI ASI ARR THR THR THR THR ASI ASI ASI ASI ARR THR THR ASI ASI ASI ASI ASI ARR ARR ARR ARR ARR ARR ARR ARR ARR AR	NUN LIRARI	AS LE AS VA TY	N U N L					ARG GLI LYS GLI PHE CTS CTS VAL ASN ASN LYS ALA PRO ALA PRO THE THE SER SER LYS		

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HEAVY	EU INDEX	OU INDEX		82	83 8	4	85 ICR 11.19.3	86 IGG2B (A)	87 IGG2B (A)	IGG2B (B)	89 IGG2B MEMB 'CL	90 MPC 11	10.1	92 IGG2A (A) 'CL	93 17/9 CL	1GG2A (B) 'CL	95 1GG2A (B)	96 IGG2A MEMB 'CL	97 MOPC 173	98 CBPC 101	99 IGA
243A 243B 243C 243C 243E 243E 243E 243F 243G 243H 243I	•	230 231										<del></del> -									
A B C	231 232 233 234	232 233 234	PRO			RO	Leu	ALA PRO  ASN LEU	ALA PRO ASN LEU	PRO  ASN		LEU	ALA PRO ASN LEU	PRO ASN LEU	ALA PRO  ASN LEU	ALA PRO  ASP LEU	ALA PRO  ASP LEU		ALA PRO  ASN LEU	ALA PRO ASP LEU	THR PRO PRO PRO PRO ILE
7 9 9 0 1 1 1 1 1 2 3	235 236 237 238 239 240	234 235 236 237 238	GLU VAL SER SER VAL		GLU VAL SER SER VAL		GLU GLY GLY PRO SER VAL	GLU GLY GLY PRO SER VAL	GLU GLY GLY PRO SER VAL	GLU GLY GLY PRO SER VAL		GLU GLY GLY PRO SER VAL	GLU GLY PRO SER VAL	GLY GLY PRO SER VAL	GLY	GLY GLY PRO SER VAL	GLY GLY PRO SER VAL		GLY GLY PRO SER VAL	GLY GLY PRO SER VAL	THR ILE PRO SER CYS GLN PRO SER
5 6 7 8 9	241 242 243 244 245 246 247 248	241 242 243 244 245 246 247	PHE PHE PRO PRO LYS PRO LYS		PHE PHE PRO PRO LYS PRO LYS		PHE ILE PHE PRO PRO ASN ILE LYS	PHE ILE PHE PRO PRO ASN ILE LYS	PHE ILE PHE PRO PRO ASN ILE LYS	PHE ILE PHE PRO PRO ASN ILE LYS		PHE PHE PRO PRO ASN ILE LYS	PHE PHE PRO PRO ASN ILE LYS	PHE PHE PRO PRO LYS ILE LYS		PHE PHE PRO PRO LYS ILE LYS	PHE ILE PHE PRO PRO LYS ILE LYS		PHE PHE PRO PRO LYS ILE LYS	ILE PHE PRO PRO LYS ILE	SER LEU GLN ARG PRO ALA LEU GLU
55 56 57 58 59	249 250 251 252 253 254 255 256 257	248 249 250 251 252 253 254 255	ASP VAL LEU THR ILE THR LEU THR		ASP THR LEU LEU ILE THR VAL THR PRO		ASP VAL LEU MET ILE SER LEU THR	ASP VAL LEU MET ILE SER LEU THR PRO	ASP VAL LEU MET ILE SER LEU THR	ASP VAL LEU MET ILE SER LEU THR		ASP VAL LEU MET ILE SER LEU THR PRO	ASP VAL LEU MET	ASP VAL LEU MET ILE SER LEU SER PRO		ASP VAL LEU MET ILE SER LEU SER	ASP VAL LEU MET ILE SER LEU SER		ASN VAL LEU MET ILE SER LEU SER	MET ILE SER LEU SER	ASP LEU LEU GLY SER ASP
71 72 73 74 75 76 77	258 259 260 261 262 263 264 265	256 257 258 259 260 261 262 263	LYS VAL THR CYS VAL VAL VAL ASP	.* ,	LYS VAL THR CYS VAL VAL VAL ASP		LYS VAL THR CYS VAL VAL VAL ASP	VAL THR CYS VAL VAL VAL ASP	LYS VAL THR CYS VAL VAL VAL ASP	PRO LYS VAL THR CYS VAL VAL VAL ASP		VAL VAL VAL VAL VAL VAL ASP		VAL VAL VAL VAL VAL VAL ASP		PROMET LEU THR CYS VAL VAL VAL ASP	PRO MET VAL THR CYS VAL VAL VAL VAL ASP		PRO ILE VAL THR CYB VAL VAL VAL ASP	VAL VAL VAL ASP	SER ILE THR CYS THR LEU ASN GLY
19 10 11 12 13 14 15 16	266 267 268 269 270 271 272 273 274	264 265 266 267 268	SER LYS ASP PRO GLU VAL GLN		SER LYS ASP ASP PRO GLU VAL		GLU ASP ASP	SER GLU ASP ASP PRO ASP VAL	SER GLU ASP ASP PRO ASP VAL	VAL SER GLU ASP ASP PRO ASP VAL		GLU ASP ASP PRO ASP VAL		SER GLU ASP ASP PRO ASP VAL		SER GLU ASP ASP PRO ASP VAL	SER GLU ASP ASP PRO ASP VAL		SER GLU ASP ASP PRO ASP VAL	ASP PRO ASP VAL	ASN PRO GLU GLY
7 8 9 0 1 2 3	275 276 277 278 279 279	270 271 272 273 274 275 276	PHE SER TRP PHE VAL		GLN PHE SER TRP PHE VAL		GLN ILE	GLN ILE SER TRP PHE VAL	GLN ILE SER TRP PHE VAL	ARG ILE SER TRP PHE VAL		PHE VAL		GLN ILE SER TRP PHE VAL		GLN ILE SER TRP PHE VAL	GLN ILE SER TRP PHE VAL		GLN ILE SER TRP PHE VAL	VAL	THR TRP GLU PRO
	281 282 283 284 285 286 287	277 278 279 280 281 282 283	VAL GLU VAL HIS THR ALA	·.	ASN VAL GLU VAL HIS THR ALA		,	VAL GLU VAL HIS THR ALA	VAL VAL VAL HIS THR	VAL GLU VAL HIS THR			e e	VAL GLU VAL HIS THR	•	ASN ASN VAL GLU VAL HIS THR	VAL GLU VAL HIS THR	ě	ASP ASN VAL GLU VAL HIS GLN	ASN ASN VAL GLU VAL HIS THR	THR GLY LYS ASP ALA VAL
	288 289 290 291 292 293 294 295 296	285 286 287 288 289 290 291 292 293	GLN THR GLN PRO ARG GLU GLU GLN PHE		GLN THR GLN PRO ARG GLU GLU GLU PHE			GLN THR GLN THR HIS ARG GLU ASP TYR	GLN THR GLN THR HIS ARG GLU ASP TYR	GLN THR GLN THR HIS ARG GLU ASP TYR				GLN THR GLN THR HIS ARG GLU ASP TYR		GLN THR GLN THR HIS ARG GLU ASP TYR	GLN THR GLN THR HIS ARG GLU ASP TYR		GLN THR THR HIS THR ARG GLN ASN TYR	ALA GLN THR GLN THR HIS ARG GLU ASP TYR	LYS LYS ALA VAL GLN ASN SER CYS
4 5 6 7 8 9 0 1 2 3	297 298 299 300 301 302	294 295 296 297 298 299 300	SER THR PHE ARG SER		ASX SER THR PHE ARG VAL			ASN SER THR ILE ARG VAL	ASN SER THR ILE ARG VAL	ASN SER THR ILE ARG VAL				ASN- SER THR LEU ARG VAL		ASN SER THR LEU ARG VAL VAL	ASN SER THR LEU ARG VAL		ASX SER THR LEU ARG VAL	SER THR LEU	CYS  TYR SER VAL
23 4 5 6 7 8 9 9 1 1 2 3	303 304 305 306 307 308 309	301 302 303 304 305 306 307 308 309	SER GLU LEU PRO ILE MET HIS		VAL SER ALA LEU PRO ILE MET			THR LEU PRO ILE GLN	VAL SER THR LEU PRO ILE GLN HIS	VAL SER ALA LEU PRO ILE GLN HIS				VAL SER ALA LEU PRO ILE GLN HIS		VAL SER ALA LEU PRO ILE GLN HIS	VAL SER ALA LEU PRO ILE GLN HIS		ALA LEU PRO ILE GLN	SER ALA LEU PRO ILE GLN	SER SER VAL LEU PRO GLY CYS
	311 312 313 314	310 311 312 313	GLN ASP TRP LEU		GLN ASP TRP LEU			HIS GLN ASP TRP MET	GLN ASP TRP MET	GLN ASP TRP MET				GLN ASP TRP MET		GLN ASP TRP MET	GLN ASP TRP MET		GLN ASN TRP MET	GLN ASP TRP MET	GLU ARG TRP ASN
4 5 6 7 9 9	315 316 317 318 319 320 321 322	314 315 316 317 318 319 320 321	ASN GLY LYS GLU PHE LYS CYS ARG	,	ASN GLY LYS GLU PHE LYS CYS ARG		SER GLY LYS GLU PHE LYS CYB LYS	SER GLY LYS GLU PHE LYS CYS LYS	SER GLY LYS GLU PHE LYS CYS LYS	SER GLY LYS GLU PHE LYS CYS LYS		SER GLY LYS GLU PHE LYS CYS LYS		SER GLY LYS GLU PHE LYS CYS LYS		SER GLY LYS GLU PHE LYS CYS LYS	SER GLY LYS GLU PHE LYS CYS LYS		SER GLY LYS GLU PHE LYS CYS LYS	SER GLY LYS GLU PHE LYS	SER GLY ALA SER PHE LYS CYB THR
	323 324 325 326 327 328 329 330	322 323 324 325 326 327 328 329	VAL ASN SER ALA ALA PHE PRO ALA		VAL ASN SER ALA ALA PHE PRO ALA		VAL ASN ASN LYS ASP LEU PRO ALA	VAL ASN ASN LYS ASP LEU PRO SER	VAL ASN ASN LYS ASP LEU PRO SER	VAL ASN ASN LYS ASP LEU PRO SER		VAL ASN ASN LYS ASP LEU PRO SER		VAL ASN ASN LYS ASP LEU PRO ALA		VAL ASN ASN ARG ALA LEU PRO SER	VAL ASN ASN ARG ALA LEU PRO SER		VAL ASN ASN LYS ASP LEU PRO ALA	ASN ASN ARG ARG LEU PRO	VAL THR HIS PRO GLU SER GLY THR
λ	331 332 333 334 335 336	330 331 332 333 334 335	PRO ILE GLU LYS THR ILE	!	PRO ILE GLU LYS THR ILE		PRO ILE GLU ARG THR ILE	PRO ILE GLU ARG THR ILE	PRO ILE GLU ARG THR ILE	PRO ILE GLU ARG THR ILE		PRO ILE GLU ARG THR ILE		PRO ILE GLU ARG THR ILE		PRO ILE GLU LYS THR ILE	PRO ILE GLU LYS THR ILE		PRO ILE GLU ARG THR ILE	PRO ILE GLU : LYS C	LEU
6	337 338 339 340	336 337 338 339	SER LYS THR LYS		SER LYS THR LYS		SER LYS PRO LYS	SER LYS ILE LYS	SER LYS ILE LYS	SER LYS ILE LYS		LYS ILE LYS		SER LYS PRO LYS		SER LYS PRO ARG	SER LYS PRO ARG		SER LYS PRO LYS	SER I	

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EU 00 100 101	102 103 104 105 106 107 10 MOPC MOPC IGE IGE IGE A IGE b IG	08 109 110 111 112 113 114 115 116 117 118 119 120 GE IGA RAT RAT IR- RAT RAT RAT RAT RAT RAT RAT IR- EMB MEMB IGM IGD 731 IGG2c IGG2a IGG1 IGG2b IGA IGE /CL IGE CL /CL /CL /CL /CL /CL /CL /CL /CL /CL /
2418	PEGION (cont'd)  102 103 104 105 106 107 118  100 107 MOPC 105 105 105 105 105 105 105 105 105 105	103   104   112   113   114   115   116   117   118   119   112   114   115   116   117   118   119   112   114   115   116   117   118   119   112   115
349 330 122	INK TIK TYR TYR TYR	THR PRO PRO PRO PRO TUB GLU GLU

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HEAVY	EU INDEX		PM3 PME5				126 127 NAB P2A2 IGG 'CL	128 39-1A, 20B	129 PA19 'CL	130 CT-12	131 132 PIRA HA-3	133 HA-11	134 HA-1	135 HA-5	136 H <b>A-1</b> :	SYRIAN HAMSTER IGM 701	136 139 GP GP' 1331 1331
243A 243B 243C 243D			===	===	===			===									
243E 243F 243G		230	VAL ASP					===	===							VAL VAL	
243H 243I 244 245	231 232	231	SER	PRO	PRC PRO	PRO PRO	PRO PRO	PRO PRO	ILE							THR	ALA PRO
245A 245B 245C 246	233	233	GLU 	GLU	GLU	GLU	GLU	GLU	===							GLU	GLX
247 248 249 250 251	234 235 236 237 238	234 235 236 237 238	LEU PRO PRO ASN VAL	LEU LEU GLY GLY PRO	LEU LEU GLY GLY PRO	LEU LEU GLY GLY PRO	LEU LEU GLY GLY PRO	LEU LEU GLY GLY PRO	GLY CYS GLN PRO							MET ASN PRO ASN VAL	LET LET GLY GLY PRO
251A 251B 252 253	239 240	239 240 241	SER VAL	SER VAL	SER VAL	SER VAL	SER VAL	SER	SER LEU							SER VAL	SER VAL
254 255 256	242 243	242	PHÉ ILE	PHE PHE	PHE ILE PHE	PRE ILE PHE	PHE PHE	PHE ILE PHE	SER LEU GLN							VAL	PHE
257 258 259	244 245 246	243 244 245	PRO PRO ARG	PRO PRO LYS	PRO PRO LYS	PRO PRO LYS PRO	PRO PRO LYS	PRO PRO LYS	ARG PRO ASP							PRO SER ARG	PRO PRO LYS
260 261 262 263	247 248 249 250	246 247 248	ASP SER PHE SER	PRO LYS ASP THR	PRO LYS ASP THR	LYS ASP THR	PRO LYS ASP THR	PRO LYS ASP THR	GLY ASP							ASP ALA PHE SER	PRC LYS ASX THR
264 265 266 267	251 252 253 254	249 250 251 252 253	GLY SER GLY THR	MET	LEU MET ILE SER	MET ILE SER	LEU MET ILE SER	MET ILE SER	LEU LEU GLY	ILE	ILE ILE SER SER	ILE	ILE	ILE	ILE	GLY PRO ALA	LEU MET ILE
268 269 270	255 256 257	255	ARG LYS SER		ARG THR PRO	ARG THR PRO	ARG THR PRO	ARG THR PRO	ARG ASP ALA	SER VAL THR PRO	SER SER LEU LEU THR THR PRO PRO	SER LEU THR PRO	SER LEU THR PRO	SER LEU THR PRO	SER LEU THR PRO	PRO ARG LYS SER	SER LEU THR PRO
271 272 273 274	258 259 260 261	256 257 258 259	ARG LEU ILE CYS		GLU VAL THR CYS	GLU VAL THR CYS	GLU VAL THR CYS	GLU VAL THR CYS	SER LEU THR CYS	GLU VAL THR CYS	GLU GLU VAL VAL SER THR CYS CYS	GLU VAL THR CYS	VAL THR CYS	GLU VAL THR CYS	GLU VAL THR CYS	ARG LEU PHE CYS	LYS ALA THR CYS
275 276 277	262 263 264 265	260 261 262	GLN ALA THR		VAL VAL VAL	VAL VAL	VAL VAL VAL ASP	VAL VAL VAL ASP	THR LEU SER	VAL VAL VAL	VAL VAL VAL VAL VAL VAL	VAL	VAL VAL VAL ASP	VAL	VAL VAL VAL ASP	GLU ALA SER	VAL VAL VAL
276 279 280	266 267	263 264 265	GLY PHE SER		ASP VAL SER	ASP VAL SER GLU G	VAL SER	SER	LEU	ASP VAL SER	ASP ASP VAL VAL SER SER		VAL SER		VAL SER	ASN PHE SER	ASP VAL SER
281 282 283 284	268 269 270 271	266 267 268	PRO LYS GLN ILE		GLN ASP ASP PRO	ASP A	SP ASP	GLU ASP ASP PRO	ASN PRO GLU ASP	GLN ASP ASP PRO	GLU GLU ASP ASP ASP ASP PRO PRO		GLN ASP ASP PRO		GLU ASP ASP PRO	PRO LYS - GLN ILE	GLN GLU ASP LEU
285 286 287 288	272 273 274 275	269	SER VAL		GLU VAL GLN PHE	GLU G VAL V GLX G PHE P	AL VAL	GLU VAL GLN PHE	ALA VAL PHE	GLU VAL GLN VAL	GLU GLU VAL VAL GLN GLN PHE PHE		GLU VAL GLN PHE		GLU VAL GLN PHE	THR	GLU VAL GLN PHE
289 290 291	276 277 278	270 271 272 273	SER TRP LEU ARG		THR TRP TYR	THR T	HR THR	THR TRP TYR	THR TRP GLU	THR TRP TYR	THR THR TRP TRP TYR TYR		THR TRP TYR			SER TRP LEU	THR TRP TYR
292 293 294 295	279	274 275	ARG ASP GLY GLN		ASN			ILE  ASN	PRO	ILE	ASP ASP		ILE			ARG ASP GLY	MET
296 297 298 299	281	276 277 278 279 280	LYS VAL GLU SER		ASN 	ASX A	SN ASN	ASN	ASN	ASP ASN  GLU	ASN ASN		ASP			LYS PRO VAL LYS	GLY ASN
300 301 302	283 284 285	281 282 283	GLY VAL LEU		GLN VAL ARG	GLN G VAL V ARG A THR T	LN GLN	GLN VAL ARG	GLY ASN GLU PRO	GLO	GLU GLU GLN GLU VAL VAL ARG ARG		GLN VAL ARG			SER GLY PHE THR	LYS LEU MET ASX
303 304 305	286 287 288	284 285	THR LYS		THR ALA ARG	ALA A	LA ALA RG ARG	THR ALA ARG	VAL GLN GLN		THR ALA ARG		THR ALA ARG			THR GLU	THR ALA GLX
306 307 308 309	289 290 291 292	286 287 288 289	PRO VAL GLU ALA		PRO PRO LEU ARG	PRO P PRO P LEU L ARG A	RO PRO EU LEU	PRO PRO LEU ARG	ARG ALA GLN ARG		PRO PRO LEU ARG		PRO PRO LEU ARG			PRO VAL THR PRO	ALA ASX VAL LEU
310 311 312 313	293 294 295 296	290 291 292 293	GLU THR LYS GLY		GLU GLN GLN PHE	GLU G GLN G GLN G PHE P	LN GLN LN GLN	GLU GLN GLN PHE	ASP LEU SER GLY		GLU GLU GLN GLN GLN GLN PHE PHE		GLU GLN GLN PHE			GLU ASP ARG GLY	GLX GLX GLX PHE
314 315 316	297 298	294 295 296 297	ALA GLY PRO ALA		ASN	ASP A		ASN	CYS		ASP ASP					SER GLY PRO	ASN
317 318 319 320	299 300 301	298 299 300	THR PHE SER		SER THR ILE ARG	SER S THR T ILE I	HR THR	SER THR ILE ARG VAL	TYR		SER SER THR THR LEU ILE					ARG THR TYR	GLY THR PHE
320 321 322 323	302 303 304	301 302 303	ILE SER SER		val Val Ser	ARG A VAL V VAL V SER S	ER SER	SER	SER VAL SER SER	VAL VAL SER	VAL VAL VAL VAL SER SER	VAL VAL SER	VAL VAL SER	VAL VAL SER	VAL VAL SER	LYS VAL ILE SER	ARG VAL VAL SER
324 325 326 327	305 306 307 308	304 305 306 307	MET LEU THR ILE		THR LEU PRO ILE	THR T LEU L PRO P ILE I ALA A	HR THR EU LEU RO PRO LE ILE	THR LEU PRO ILE	VAL LEU PRO SER	THR LEU PRO ILE	THR THR LEU LEU PRO PRO ILE ILE	THR LEU PRO ILE	ILE LEU PRO ILE	ILE LEU PRO ILE	THR LEU PRO ILE	THR LEU THR ILE	ALA LEU THR ILE
328	309 310 311 312	308 309 310 311	THR GLU SER		THR	ALA A HIS H GLU G ASP A TRP T	LA ALA IS HIS LN GLU	ALA HIS GLU	SER ALA GLU	ILE ALA HIS GLU	ALA ALA	ILE ALA HIS GLU ASP	HIS	HIS	LYS HIS GLU	THR GLU SER	GLX HIS ASX
330 331 332 333	313 314	313	ASP TRP LEU		ASP TRP LEU			ASP TRP LEU	THR TRP LYS	ASP TRP LEU	HIS HIS GLU GLU ASP ASP TRP TRP LEU LEU	ASP TRP LEU	GLU ASP TRP LEU	ASP TRP LEU	ASP TRP LEU	ASP TRP LEU	TRP
334 335 336	315 316 317	314 315 316	SER GLN SER		ARG GLY LYS	ARG AL	YS LYS	ARG GLY LYS	ALA ARG THR	ARG GLY LYS	LYS ARG GLY GLY LYS LYS	ARG GLY LYS	SER GLY LYS	SER GLY LYS	ARG GLY LYS	ASN LEU SER	
337 338 339 340	318 319 320 321	317 318 319 320 321	LEU TYR THR CYS		GLU PHE LYS CYS	GLU GI PHE PI LYS LI CYS CI	LU GLU HE PHE YS LYS YS CYS	GLU PHE LYS CYS	GLU PHE THR CYS		GLU PHE LYS CYS		GLU PHE LYS CYS			VAL TYR THR CYS	
341 342 343	322 323 324 325	321 322 323 324	ARG VAL ASP HIS		LIS	VAL VI HIS HI ASP AS LYS LY	12 L12	LYS VAL HIS	THR VAL THR		CYS LYS VAL HIS		LYS VAL HIS			ARG VAL ASP	
343 344 345 346 347	326 327 328	326	ARG GLY ILE		ASN LYS ALA LEU	ASP AS LYS LY ALA AS LEU LE	LA ALA	ASN LYS ALA LEU	HIS PRO GLU ILE		ASP LYS ALA ALA LEU LEU		ASP LYS ALA			HIS ARG GLY	
347 348 349 350 351	329 330 331 332	327 328 329 330 331	PHE PHE ASP LYS		PRO ALA PRO ILE	PRO PI ALA AI PRO PI ILE II	RO PRO LA ALA RO PRO LE ILE	PRO ALA PRO ILE	ASP SER GLY SER		PRO PRO ALA SER PRO ILE		LEU			LEU THR PHE TRP LYS	ILE ILE
351A 352 353 354 355	333 334 335 336	332 333 334 335	ASN VAL SER MET		THE	GLU GI LYS LY THR TH	U GLU S LYS IR THR	GLU LYS THR	LEU THR ALA THR		GLU LYS THR					ASN VAL SER	THR THR ARG ARG THR THR
356 357 358	337 338 339	336 337 338	SER SER GLU CYS		ILE SER LYS	SER SE	R SER	ILE SER LYS	ILE SER ARG GLY		ILE SER LYS					SER	ILE ILE SER SER
359 360	339 340	339	SER THR		ALA ARG	LYS LY ALA AI ARG AF	A ALA	LYS ALA ARG			ALA LYS					ALA	LYS LYS ALA ALA LYS LYS

HÈA	AX COS	START	CHAINS	CH2	REGION	(cont'	2)										
	EU Indi	X IND	EX GP IGG2	141 MOO	142 143 PIG SHEEP IGG PSHC	HORSE IGG	145 BOVINE IGG	146 GOAT IGG	CHICKE IGM 'CL	EN Eloj VH	8 149 ps Re41 'CL	150 Re20	151 Xenopus laevis IgY	152 S Xenopus laevis c8(II)	153 Xenopus laevis cl4(II)	154 Xencpus laevis c35	X
2437 2438 2430 2430	9									===	===		===	===			-
243F 243F		230 231		VAL					ile	GLU		: :::	CYS	PRO			
243H 2431 244 245	231	231		MET	PRO PRO				FRO	PRO	O VAI		GLN ASP GLU	LYS PRC			
245 2458 2458 2450 246	233	233			GLU				PRO	LYS	===		PRO				
247 248 249	234 235 236 237	234 235 236 237	ASN LEU GLY	LEU PRO PRO	LEU PRO GLY				ASN GLY ILE	PRO PRO ARG	HIS	PRO	GLU PRO ILE	VAL GLU LYS PRO			
250 251 251A 251B	238	238		VAL	GLY PRO				PRC LEU	PRO	VAL	PRO	GLÜ PRO	VAL VAL			
251A 251B 252 253 254 255	239 240 241 242	239 240 241 242	SER VAL PHE ILE	GLY PHE	SER VAL PHE ILE				PHE VAL THR	VAL LEU SER	THR	GLN LEU ILE	THR VAL GLU	SER ILE HIS			
255 256 257 258 259	243 244 245 246	243 244 245	PHE PRO PRO LYS	PRO PRO	PHE PRO PRO LYS				MET HIS PRO PRO	MET THR		LEU	LEU GLN	PRO PRO SER			
260 261 262 263	247 248 249 250 251	246 247 248	PRO LYS ASP	ASP ALA	PRO LYS ASP				SER ARG GLU ASP	PRO SER GLN GLU	ALA LEU ASP	PRO SER PRO GLU	GLY PRO CYS ALA	LYS ASP ALA LEU			
264 265 266 267	251 252 253 254 255	249 250 251	THR LEU MET. ILE SER I	PHE	THR LEU THR ILE				PHE GLU GLY PRO	GLU LEU THR LEU	GLU	THR LEU HIS ASN	SER SER Lys	ALA LEU ASN			
269	254 255 256 257	251 252 253 254 254	SER I LEU I THR I	ARG Lys	SER GLY THR PRO				PHE ARG ASN	ASN LYS THR	GLN GLY LYS	GLN THR THR	SER VAL GLU LEU	GLU SER LEU PHE			
270 271 272 273 274	258 259 260 261	255 256 257 258 259	ARG I VAL I THR I	PRO LEU I LE	GLU VAL THR CYS				ALA SER ILE LEU	ALA THR PHE ALA	ALA VAL	ALA VAL LEU GLY	LEU	ILE			
275 276 277 278	262 263 264	260 261 262	VAL O VAL A VAL S	GLN ALA SER	VAL VAL VAL				GLN THR ARG	LEU ALA THR	LEU VAL ASN	MET ILE SER	CYS LEU ILE THR	CYS LEU ALA THR			
279 280 281 282	265 266 267 268	263 264 265 266	ASP C VAL E SER S GLN E	PHE SER PRO	ASP VAL GLY GLN				GLY ARG ARG ARG	ASP PHE TYR PRO	ASP PHE THR PRO	GLY PHE SER PRO	GLY TYR ALA PRO	ASN PHE THR			
282 283 284 285	269 270 271 272	267 268	ASP A GLU G PRO -	ARG SLN	ASP ASP PRO GLU				PRO THR	LYS GLY HIS	ALA ILE PHE	asp asn Ile	SER GLU ILE	PRO THR HIS ILE			
286 287 288 289	273 274 275 276	269 270	VAL V GLN -		VAL GLN PHE SER				GLU VAL THR	SER PHE  LYS	THR VAL  ASN	LYS VAL SER	VAL	VAL ILE			
290 291 292 293	277 278 279	271 272 273 274	TRP S PHE L VAL A	ER EU RG	TRP PHE VAL				TRP TYR LYS	TRP LEU ARG	TRP LEU LYS	TRP LYS	HIS TRP LEU LEU	LYS TRP LEU LYS			
294 295 296 297	280 281	275 276 277 278 279	ASP L ASN G	YS LN	ASP ASN		-		ASN GLY SER PRO	ASP GLY LYS GLU	ASN GLY LYS PRO	ALA GLY LEU ASN	ASN GLY GLN VAL	asn Gly Asn Gln			
298 299 300 301	282 283 284	279 280 281 282	LYS S PRO G VAL V	LU ER LY	VAL GLU				VAL	VAL THR ASP GLY	ASP SER GLY	GLN ALA GLY VAL	THR ASN ILE SER	THR THR GLU GLY			
302 303 304	285 286 287	283 284	GLY T ASN - ALA T	HR HR	VAL ARG THR ALA					ALA	VAL	LEU	PRO SER ASN	VAL ARG VAL			
305 306 307 308 309	288 289 290 291 292	285 286 287 288 289	GLU A THR G LYS V PRO G	LU AL LX	ARG THR LYS PRO				ALA ALA ALA	THR LEU THR GLU	THR SER PRO ALA	PRO SER THR PRO	SER LYS PRO CYS	GLU GLU PRO VAL			
310 311 312 313	293 294 295 296	290 291 292 293	VAL G GLU A GLN L TYR G	LX LA YS	ARG GLU GLU GLN PHE				ALA THR THR ALA THR	CYS GLN LYS LYS GLY	PHE GLN VAL ASN GLY	ARG THR ASN GLY GLY	LYS GLU GLU ASN GLY	GLU ASP LYS LYS ARG			
314 315 316 317	297 298	294 295 296 297	ASN SI	LY RO	ASN				THR VAL GLY	ASP LYS	THR GLY	===	THR PHE SER	GLY TYR GLU			
318 319 320 321	299 300	298 299 300	THR THE TO ARG LOVAL VALVA	ir	SER THR PHE ARG				PRO GLU VAL VAL ALA	SER PHE THR ALA	ASN	PHE GLU THR	SER ARG SER LYS	ALA THR SER			
322 323 324 325	301 302 303 304 305	301 302 303 304	SER SI	<b>CR</b>	VAL VAL SER ALA				GLU Ser	SER SER PHE LEU	THR SER GLN	VAL ALA TYR LEU	VAL SER VAL	TYR LEU SER ILE			
326 327 328	306 307 308 309	305 306 307 308	VAL ME LEU LE PRO TE ILE II GLN GI	æ	LEU PRO ILE GLN				ARG ILE SER VAL THR	GLN ALA SER GLU	THR PHE THR	PRO LEU ASN VAL	PRO LYS GLU ASP TRP	THR ARG LYS GLU TRP			
329 330 331 332 333	310 311 312 313 314	309 310 311 312 313	HIS GL GLN GL ASP AL TRP TR LEU LE	N A P	HIS GLN ASP TRP THR				GLU SER GLU TRP ASP	SER GLN TRP LYS ARG	GLU GLU TRP PHE	GLU GLU TRP THR	ASN SER GLU ASP	ASP LEU ASP THR			
334 335 336	315 316 317	314 315 316	ARG SE	R N	GLY				THR GLY	LEU		ASN  LYS	SER  TYR THR	LEU  TYR SER			
337 338 339	318 319 320	317 318 319	LYS SE GLU VA PHE PH LYS TH CYS CY LYS LY	K L E R	LYS GLU PHE LYS				ALA THR PHE SER	GLY THR PHE THR	VAL TYR	GLN GLU TYR	CYS LYS VAL	CYS VAL VAL			
340 341 342 343	321 322 323 324	320 321 322	CYS CY LYS LY VAL VA TYR GLI ASN HI	8 5 L	CYS LYS VAL				VAL VAL	CYS GLN PHE	GLN (	TYS SLU /AL	THR HIS PRO ALA	GLU HIS ALA GLU			
344 345 346 347	324 325 326 327	322 323 324 325 326	ALA GL	Y	HIS ASN GLU ALA				MET	ILE GLN GLU GLY	ASN THIS I	HR HIS LA PRO	SER HIS THR LYS	SER GLY SER LEU			
347 348 349 350	328 329 330 331 332	327 328 329 330 331	PRO THE PRO GLE PRO GLE ILE GLE	e N	LEU PRO ALA PRO TLE				asn Thr Ser	GLU ILE THR GLU	ASP S LEU C LYS E SER S	HE ER	GLU ALA	GLN GLU LYS ASN			
351 <b>A</b> 352 153	333 334 335	332 333	GLU ASI LYS ALI THR SEI	_	ILE VAL ARG				LYS ARG MET	GLN THR VAL LYS	GLN A	SP S	SER	MET SER LYS			
354 355 356 357	336	334 335 336 337	ILE SEF	•	THR ILE SER				GLU CYS GLY LEU	TYR SER SER ALA	ILE I SER A MET H PRO A	Le . Sn i et i	LYS	SER LEU MET CYS			
358 359 360	338 339 340	338 339	LYS THE THR SEE LYS		ARG THR LYS				GLU ( PRO	GLU	PRO T	YR 🌶	ASP .	ASP THR			

HEA	EU INI	017	HAINS CE 156 K Xenopus	157	150		• OF SEQUEN	CES AMI	F OCCURRENCES NO OF MOST COMMON DS AMINO ACID	VARIABILI
2438			X Xenopus laevis J2(I) 'CL	J4 (III)	J6(I)	J12(IV)				
243E 243E 243C 243C 243E	,						4 4 5 5	1 1 1 1 1 1	4 (VAL) 4 (PRO) 4 (SER) 5 (THR) 5 (PRO)	
243F 243G 243H 243I		230 231 232					35 36	1 8	5 (PRO) 18 (VAL) 8 (VAL)	
244 245	231 232						40 63 59	8 9 6 5 2	11 ( + ) 37 (ALA) 45 (PRO)	10. 6.6
245A 245B 245C 246	3	233					9 9 12 91	2 1 2 10	5 (THR) 9 (PRO) 9 (PRO) 44 (GLU), 41 (GLU)	
247 248 249 250	234 235 236	234 235 236 237					95 96 96 95 94	12 13 8	48 (LEU) 36 (LEU) 43 (GLY)	21.,22. 24. 35. 16.
251 251A	238	237 238					95 94 12	12 6 1	44 (GLY) 54 (PRO) 12 (CYS)	26. 10.
251B 252 253 254	241	239 240 241					12 12 97 97 96	2 8 8 11	8 (HIS) 60 (SER) 73 (VAL) 62 (PHE)	13. 11. 17.
255 256 257 258 259	242 243 244 245 246	242 243 244					94 76 94	a . 9	36 (ILE)	21. 9.7 1213.
260 261	247	245 246 247 248					93 94 94 96	10	41 (LYS)	27.,30. 21.,23.
263 264	248 249 250 251	249					96 85 96	10,1 10,1 8 12	29 (THR) 66 (LEU)	21.,23. 13.,14. 35. 10.
265 266 267 268	252 253 254 255 256	250 251 252 253 254					97 103 101 99	10,1 10,1	1 41 (MET) 1 53 (ILE) 47 (SER)	26. 19.,21. 21. 29.
269 270 271	256 257 258 259	254 255. 256 257					99 97 97	11 9 5 11	38 (ARG) 57 (THR) 48 (PRO)	10.
271 272 273 274	261	258 259					98 98 98	5 9 1	31 (GLU) , 29 (GLU) 47 (VAL) 65 (THR) 98 (CYS)	34.,37. 10. 14. 1.
275 276 277 278 279	262 263 264 265	260 261 262 263					99 97 97 96	7 5 7 3	49 (VAL) 59 (VAL) 50 (VAL) 48 (ASP)	14. 8.2 14. 6.
280 281 282	266 267 268 269 270	264 265 266 267					96 94 85 84	8 9 9	42 (VAL) 54 (SER) 20 ( + ) 27 (ASP)	10. 16.
283 284 285	2/1	268					84 85 82 93	9 9 10	47 (ASP) 51 (PRO)	28. 16. 14.
286 287 288 289	272 273 274 275 276	269 270					93 70 75	7,8 6 8	34 (GLU) , 32 (GLU) 73 (VAL) 36 (GLN) , 34 (GLN) 48 (PHE) 30 (SER)	27.,29. 7.6 14.,16.
290 291 292 293	277 278 279	271 272 273 274					94 93 94	. 4 8 9	30 (SER) 79 (TRP) 28 (TYR) 37 (VAL) 10 (ASP)	25. 4.7 27. 23.
293 294 295 296 297	280 281	275					94 22 22 90	5 2 11	21 (GLI)	2.1
298 299	282	277 278 279 280					94 30 22 93	11 7 8,9	27 (ASN), 25 (ASN) 16 (VAL) 7 (GLU) 35 (VAL)	32.,33. 38.,41. 13. 25. 21.,24.
300 301 302 303	283 284 285 286	281 282 283					91 91 91 59	10 9 13	33 (GLU) , 32 (GLU) 57 (VAL) 30 (HIS)	28. 14. 39.
304 305 306	286 287 288 289	284 285 286					91 92	5 7 12 11	23 (THR) 42 (ALA) 22 (LYS)	13. 15. 50.
307 308 309 310	290 291 292 293	287 288 289					92 91 91	11 11 15	34 (THR) 19 ( + ) 24 (PRO) 39 (ARG)	30. 53. 42. 35.
311 312 313	294 295 296	290 291 292 293					91 91 91 91	11 12,13 9,10	51 (GLU) , 46 (GLU) 28 (GLU) , 26 (GLU) 33 (GLN) , 31 (GLN) 26 (GLY)	14.,16. 36.,38. 33.,38. 31.,35.
314 315 316 317	297 298 299	294 295 296 297					87 32 32 75	9 8 5	40 (ASN) , 34 (ASN) 12 (GLU) 15 (PRO)	20.,23. 21. 11.
318 319	300	298 299 300					76 91	10 6 10	56 (THR)	19. 8.1 25.
320 321 322 323	301 302 303 304 305	301 302 303					90 96 96 95	8 7 10 6	36 (TYR) 39 (ARG) 73 (VAL) 45 (VAL) 90 (SER)	18. 9.2 21. 6.3
324 325 326 327 328	306 307 308 309	304 305 306 307					96 96 97 97	11 7 10 9	30 (VAL) 90 (LEU) 41 ( + ) 52 (ILE)	35. 7.5 24. 17.
129 130 131 132	310 311 312	308 309 310 311					97 97 96	12	15 (GLN) , 14 (GLN)	17.
,,,	314	311 312 313					94 95 95	11 5 9	49 (GLN) , 46 (GLN) 53 (ASP) , 51 (ASP) 90 (TRP) 54 (LEU)	16.,17. 20. 5.3 16.
34 35 36 37	315 316 317 318	314 315 316 317					94 96 98	11 9 11	35 (SER) 63 (GLY) 51 (LYS)	30. 14. 21.
38 39 40 41	319 320 321 322	318 319 320 321					93 93 92 92 92	8 3 5 2	42 (GLU) 56 (PHE) 46 (LYS) 90 (CYS)	18. 5. 10. 2.
42 43 44 45	323 324 325 326	322 323 324 325 326					92 93 92 93	8 5 9 7	48 (LYS) 77 (VAL) 20 ( + )	15. 6. 42.
46	326 327 328 329 330	325 326 327					94	9	20(+) 35(ASN) 35(LYS) 34(GLY) 61(LEU)	18. 24. 25. 18.
50 51	330 331 332	327 328 329 330 331					94 94 87 79	12 10 8 9 7	46 (PRO) 31 (ALA) 49 (PRO) 44 (ILE)	20. 24. 16.
51A 52 53 54 55	333 334 335 336	332 333 334					3 95 96 95	3 10 10	1 ( + ) 41 (GLU)	23. 26.
6	336 337 338	335 336 337 339					34	9 7 6	37 (LYS) 66 (THR) 56 (TLE) 10 (MET)	13. 12. 20.
8	338 339 340	336 339					95 96 74 61	12 8 7	48 (SER) 58 (LYS) 23 (ALA) 34 (LYS)	16. 20. 26. 13.
									,,	13.

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